

after chronic exposure to moderate and high levels of NH<sub>3</sub>. An individual assessment was implemented wherein shrimp hemolymph metabolite profiles were assessed pre- and post-exposure to identify individual responses to 0 ppm (control), 10 ppm and 20 ppm NH<sub>3</sub> across a 72 h period. Key metabolites that have previously been linked to condition and stress responses in penaeid shrimp were quantified, including total protein, glucose, triglycerides, and hemocyanin. Additionally, shrimp were held in individual respirometers throughout the trial and the oxygen consumption of shrimp was measured with fiber optic probes as a proxy of activity, or metabolism. Oxygen consumption in response to NH<sub>3</sub> exposure showed wide variance in controls, while shrimp exposed to 10 ppm and 20 ppm NH<sub>3</sub> decreased oxygen consumption in the 24 h period post-exposure. After 48h shrimp exposed to 10 ppm showed evidence of recovery through increased oxygen consumption, while 20 ppm remained low. Hemolymph triglycerides at 96 h post-exposure are significantly decreased in shrimp exposed to 20 ppm NH<sub>3</sub> compared to 10 ppm and control shrimp, indicating an increase in energy expenditure. Other biochemical parameters measured including total protein, hemocyanin and glucose decreased pre- to post exposure due to feed restriction, and were not significantly different between treatments. To complement physiological data, the transcriptomic profile of gill tissue from shrimp post-exposure were obtained by Illumina RNASeq. Differentially expressed genes were identified in response to NH<sub>3</sub> exposure, as well as in shrimp that showed physiological evidence of recovery. The pathways enriched and genes co-expressed were identified and demonstrate how shrimp respond to ammonia stress, and potentially how some animals are able to tolerate NH<sub>3</sub>.

**keywords:** Transcriptomics, physiology, stress, aquaculture, shrimp

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#### P-068.

##### **CqSIRT1 from red claw crayfish *Cherax quadricarinatus* promotes white spot syndrome virus infection VIA positively regulating PI3K-AKT-mTOR pathway**

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#### Abstract

Sirtuins (SIRT) are a family of evolutionarily conserved nicotinamide adenine dinucleotide (NAD<sup>+</sup>)-dependent deacylases that participate in antiviral immunity. In this report, the *SIRT1* gene (named as *CqSIRT1*) was identified with an open reading frame of 2256 bp that encoding 751 amino acids from red claw crayfish *Cherax quadricarinatus*. Tissue distribution analysis showed that *CqSIRT1* was ubiquitously expressed in all tissue tested with high expression in haematopoietic tissue (Hpt), haemocyte and gill, while low expression in hepatopancreas, muscle and eyestalk. Unexpectedly, dysfunction of *CqSIRT1* by gene knockdown in red claw crayfish Hpt cell cultures resulted in markedly decrease expression of an early gene *ie1* and an envelope protein gene *vp28* of white spot syndrome virus (WSSV) at late stages post WSSV infection, indicating that *CqSIRT1* was hijacked by WSSV to promote its replication. Importantly, the expression of *PI3K*, *AKT* and *mTOR*, which were involved in energy metabolism and autophagy, was significantly reduced after gene silencing of *CqSIRT1* during WSSV infection. Overall, these data suggest that *CqSIRT1* could promote WSSV replication through positively modulating PI3K-AKT-mTOR signaling pathway in red claw crayfish *C. quadricarinatus*, which benefits further understanding of the molecular mechanism underlying the pathogenesis of WSSV in crustacean.

**keywords:** Sirtuins 1 (SIRT1); PI3K-AKT-mTOR; White spot syndrome virus (WSSV); Haematopoietic tissue (Hpt); *Cherax quadricarinatus*.

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#### P-069.

##### **The role of CD8 $\alpha$ in the immune response of sea bass against nodavirus**

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#### Abstract

The adaptive immune response is mediated by different mechanisms including humoral factors, cellular elements (T and B lymphocytes) and other specific proteins as major histocompatibility complex which act in coordination with diversified antigen receptors. Regarding cytotoxic T cells (CTLs) of vertebrates, they are direct effector lymphocytes in the fight against virus-infected cells by killing their cellular targets. The cluster of differentiation 8 $\alpha$  (CD8 $\alpha$ ) is the distinctive marker of the lymphocyte subset of cytotoxic CTLs. However, teleost CTLs function is largely unknown mainly because of the lack of population-specific antibodies. European sea bass (*Dicentrarchus labrax*) is a very susceptible species to nodavirus (NNV) in which causes devastating mortality rates and, up to date, no solutions are available to prevent them. Previous studies pointed to the relevance of cell-mediated cytotoxicity in the response of European sea bass juveniles against NNV at transcriptional level. Thus, we have investigated the distribution, production and potential role on European sea bass CD8 $\alpha$ <sup>+</sup> cells by flow cytometry using a polyclonal antibody against European sea bass CD8 $\alpha$  in naïve and NNV-infected cells. This work represents the first attempt to characterize CD8 $\alpha$ <sup>+</sup> cells in European sea bass.

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**keywords:** *Dicentrarchus labrax*, nodavirus, CD8 $\alpha$ , polyclonal antibodies.

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#### P-070.

##### **Study of the immunomodulatory and antiviral activity of bacterial lipopolysaccharides in seabass (*Dicentrarchus labrax*, Linnaeus 1758)**

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